

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/547,532

Source:

PT/10

Date Processed by STIC:

9/13/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

*pp 1-10*

3 <110> APPLICANT: SHINTANI, ET AL.  
 5 <120> TITLE OF INVENTION: MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING  
 BRAIN/NERVE  
 6 CELL PROTECTIVE AGENT  
 8 <130> FILE REFERENCE: 20039.1USWO  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/547,532  
 C--> 11 <141> CURRENT FILING DATE: 2005-08-31  
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/002774  
 14 <151> PRIOR FILING DATE: 2004-03-04  
 16 <150> PRIOR APPLICATION NUMBER: JP 2003-056885  
 17 <151> PRIOR FILING DATE: 2003-03-04  
 19 <150> PRIOR APPLICATION NUMBER: JP 2003-106247  
 20 <151> PRIOR FILING DATE: 2003-04-10  
 22 <160> NUMBER OF SEQ ID NOS: 21  
 24 <170> SOFTWARE: PatentIn version 3.1

*Suggestion: Consult  
sequence rules  
for valid format*

*Does Not Comply  
Corrected Diskette Needed*

## ERRORED SEQUENCES

26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 288  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Homo sapiens  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(288)  
 34 <223> OTHER INFORMATION:  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: sig\_peptide  
 38 <222> LOCATION: (1)..(78)  
 39 <223> OTHER INFORMATION:  
 W--> 41 <220>  
 42 <221> NAME/KEY: mat\_peptide  
 43 <222> LOCATION: (79)..()  
 44 <223> OTHER INFORMATION:  
 W--> 46 <400> 1  
 W--> 47 atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg 48Met Cys  
 E--> 48 Cys thr Lys ser Leu Leu Leu ala ala Leu met ser val Leu -25  
 W--> 49 -20 -15 cta ctc cac ctc tgc ggc gaa tca  
 W--> 50 gaa gca gca agc aac ttt gac tgc 96Leu Leu His Leu Cys Gly Glu Ser Glu Ala  
 E--> 51 ala ser asn Phe asp cys -10 -5 -1 1  
 W--> 52 5 tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc  
 W--> 53 144Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly  
 W--> 54 10 15 20 ttc aca cgg cag ctg

*Amino acid  
numbers are  
completely  
misaligned*

*Cumulative base  
totals are at  
right margin of each line.*

*Insert a  
hard return.*

*Amino acids go directly  
under their  
codons.*

*invalid format*

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

*same end*

```

W--> 55 gcc aat gaa ggc tgt gac atc aat gct atc atc      192Phe Thr Arg Gln Leu Ala Asn
E--> 56 glu gly cys asp Ile asn ala Ile Ile      25      30
W--> 57 35      ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa
W--> 58 cag act      240Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
W--> 59 40      45      50      tgg gtg
W--> 60 aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg      288Trp Val Lys Tyr
E--> 61 Ile val arg Leu Leu ser Lys Lys val Lys asn met      55      60
E--> 62 65      70

```

```

83 <210> SEQ ID NO: 3
84 <211> LENGTH: 288
85 <212> TYPE: DNA
86 <213> ORGANISM: Rattus norvegicus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (1)..(288)
91 <223> OTHER INFORMATION:
93 <220> FEATURE:
94 <221> NAME/KEY: sig_peptide
95 <222> LOCATION: (1)..(75)
96 <223> OTHER INFORMATION:

```

```

W--> 98 <220>
99 <221> NAME/KEY: mat_peptide
100 <222> LOCATION: (76)..()
101 <223> OTHER INFORMATION:

```

*same ends*

```

W--> 103 <400> 3
W--> 104 atg gcc tgc aag cat ctg ccc ttc ctg gct ttg gcg ggg gta ctg ctg      48Met Ala
E--> 105 cys Lys his Leu Pro Phe Leu ala Leu ala gly val Leu Leu      -25
E--> 106 -20      -15      -10
W--> 107 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc      96Ala Tyr
W--> 108 Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
W--> 109 -5      -1 1      5      ctc acg tac aca aag aac
W--> 110 gtg tat cat cat gcg aga aat ttt gtg ggt      144Leu Thr Tyr Thr Lys Asn Val Tyr
E--> 111 his his ala arg asn Phe val gly      10      15
W--> 112 20      ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct
W--> 113 atc atc      192Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
W--> 114 25      30      35      ttt cac ctg
E--> 115 aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc      240Phe His Leu Lys Ser
W--> 116 Lys arg ser val cys ala asp Pro Lys gln Ile      40      45
W--> 117 50      55      tgg gtg aaa agg att ttg cac ctc ctc agc cta aga
W--> 118 acc aag aag atg      288Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys
E--> 119 Lys met      60      65      70

```

```

140 <210> SEQ ID NO: 5
141 <211> LENGTH: 291
142 <212> TYPE: DNA
143 <213> ORGANISM: Mus musculus
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(291)
148 <223> OTHER INFORMATION:

```

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

```

150 <220> FEATURE:
151 <221> NAME/KEY: sig_peptide
152 <222> LOCATION: (1)..(81)
153 <223> OTHER INFORMATION:
W--> 155 <220>
156 <221> NAME/KEY: mat_peptide
157 <222> LOCATION: (82)..()
158 <223> OTHER INFORMATION:
W--> 160 <400> 5
W--> 161 atg gcc tgc ggt ggc aag cgt ctg ctc ttc ctt gct ttg gca tgg gta      48Met Ala
E--> 162 cys gly gly Lys arg Leu Leu Phe Leu ala Leu ala trp val      -25
W--> 163 -20      -15      ctg ctg gct cac ctc tgc agc cag gca
W--> 164 gaa gca gca agc aac tac gac      96Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala
E--> 165 ala ser asn tyr asp      -10      -5      -1 1
W--> 166 5      tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg
W--> 167 144Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
W--> 168 10      15      20      ggt ttc aca aga cag atg
W--> 169 gcc gat gaa gct tgt gac att aat gct atc      192Gly Phe Thr Arg Gln Met Ala Asp
E--> 170 glu ala cys asp Ile asn ala Ile      25      30
W--> 171 35      atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag
W--> 172 cag      240Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
W--> 173 40      45      50      aac tgg gtg aaa
W--> 174 agg gct gtg aac ctc ctc agc cta aga gtc aag aag      288Asn Trp Val Lys Arg Ala
E--> 175 val asn Leu Leu ser Leu arg val Lys Lys      55      60
W--> 176 65      atg
E--> 177 291met      70
200 <210> SEQ ID NO: 7
201 <211> LENGTH: 1122
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (1)..(1122)
208 <223> OTHER INFORMATION:
W--> 210 <400> 7
W--> 211 atg agc ggg gaa tca atg aat ttc agc gat gtt ttc gac tcc agt gaa      48Met Ser
E--> 212 gly glu ser met asn Phe ser asp val Phe asp ser ser glu      1
W--> 213 5      10      15      gat tat ttt gtg tca gtc
W--> 214 aat act tca tat tac tca gtt gat tct gag      96Asp Tyr Phe Val Ser Val Asn Thr
E--> 215 ser tyr tyr ser val asp ser glu      20      25
W--> 216 30      atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta
W--> 217 ttt      144Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
W--> 218 35      40      45      gta ccg att gcc
W--> 219 tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat      192Val Pro Ile Ala Tyr Ser
E--> 220 Leu Ile cys val Phe gly Leu Leu gly asn      50      55
W--> 221 60      att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc
W--> 222 agg tct atg      240Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser
E--> 223 met      65      70      75      80
W--> 224 aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt      288Thr Asp

```

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

W--> 225 Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val *same*  
W--> 226 85 90 95 ctt act ctc cca ttc tgg  
W--> 227 gca gtg agt cat gcc act ggt gcg tgg gtt 336Leu Thr Leu Pro Phe Trp Ala Val  
E--> 228 ser his ala thr gly ala trp val 100 105  
W--> 229 110 ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc  
W--> 230 aac 384Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn  
W--> 231 115 120 125 ttt aac tgc ggg  
W--> 232 atg ctg ctc ctg act tgc att agc atg gac cgg tac 432Phe Asn Cys Gly Met Leu  
E--> 233 Leu Leu thr cys Ile ser met asp arg tyr 130 135  
W--> 234 140 atc gcc att gta cag gcg act aag tca ttc cgg ctc cga  
W--> 235 tcc aga aca 480Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg  
E--> 236 thr 145 150 155 ttt aac tgc ggg  
W--> 237 cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc 528Leu Pro  
W--> 238 Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val  
W--> 239 165 170 175 atc atc tcc agc tca act  
W--> 240 ttt gtc ttc aac caa aaa tac aac acc caa 576Ile Ile Ser Ser Ser Thr Phe Val  
E--> 241 Phe asn gln Lys tyr asn thr gln 180 185  
W--> 242 190 ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tgc gag ccc  
W--> 243 atc 624Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile  
W--> 244 195 200 205 agg tgg aag ctg  
W--> 245 ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt 672Arg Trp Lys Leu Met  
E--> 246 Leu gly Leu glu Leu Leu Phe gly Phe Phe 210 215  
W--> 247 220 atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att  
W--> 248 gtc aaa acc 720Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys  
E--> 249 thr 225 230 235 240  
W--> 250 ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc 768Leu Val  
W--> 251 Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile  
W--> 252 245 250 255 ata gct gtg gtg ctt gtg  
W--> 253 ttt ctg gct tgt cag att cct cat aac atg 816Ile Ala Val Val Leu Val Phe Leu  
E--> 254 ala cys gln Ile Pro his asn met 260 265  
W--> 255 270 gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc  
W--> 256 tgc 864Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys  
W--> 257 275 280 285 cag agc gaa aag  
W--> 258 cta att ggc tat acg aaa act gtc aca gaa gtc ctg 912Gln Ser Glu Lys Leu Ile  
E--> 259 gly tyr thr Lys thr val thr glu val Leu 290 295  
W--> 260 300 gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct  
W--> 261 ttt att ggg 960Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile  
E--> 262 gly 305 310 315 320  
W--> 263 cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt 1008Gln Lys  
W--> 264 Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys  
W--> 265 325 330 335 gtg aga agg aag tac aag  
W--> 266 tcc tca ggc ttc tcc tgt gcc ggg agg tac 1056Val Arg Arg Lys Tyr Lys Ser Ser  
E--> 267 gly Phe ser cys ala gly arg tyr 340 345  
W--> 268 350 tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac  
W--> 269 aat 1104Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn  
W--> 270 355 360 365 gcg tgc tcc ttc  
W--> 271 act atg 1122Ala Ser Ser Phe Thr Met  
E--> 272 370

329 &lt;210&gt; SEQ ID NO: 9

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set : N:\CRF4\09132005\J547532.raw

330 &lt;211&gt; LENGTH: 1101

331 &lt;212&gt; TYPE: DNA

332 &lt;213&gt; ORGANISM: Mus musculus

334 &lt;220&gt; FEATURE:

335 &lt;221&gt; NAME/KEY: CDS

336 &lt;222&gt; LOCATION: (1)..(1101)

337 &lt;223&gt; OTHER INFORMATION:

W--> 339 <400> 9

W--> 340 atg aat tcc aca gag tcc tac ttt gga acg gat gat tat gac aac aca 48Met Asn

E--> 341 ser thr glu ser tyr Phe gly thr asp asp tyr asp asn thr 1

W--> 342 5 10 15 gag tat tat tct att cct

W--> 343 cca gac cat ggg cca tgc tcc cta gaa gag 96Glu Tyr Tyr Ser Ile Pro Pro Asp

E--> 344 his gly Pro cys ser Leu glu glu 20 25

W--> 345 30 gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta

W--> 346 ata 144Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile

W--> 347 35 40 45 tgt gtc ttt ggc

W--> 348 ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc 192Cys Val Phe Gly Leu Leu

E--> 349 gly asn Ile met val val met thr Phe ala 50 55

W--> 350 60 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg

W--> 351 ttg aac atg 240Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn

E--> 352 met 65 70 75 80

W--> 353 gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288Ala Ile

W--> 354 Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val

W--> 355 85 90 95 act cat gcc acc aac act

W--> 356 tgg gtt ttc agc gat gca ctg tgt aaa ctg 336Thr His Ala Thr Asn Thr Trp Val

E--> 357 Phe ser asp ala Leu cys Lys Leu 100 105

W--> 358 110 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc

W--> 359 ctg 384Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu

W--> 360 115 120 125 gcc tgt atc agc

W--> 361 atg gac cgg tac att gcc atc gtc cag gca acc aaa 432Ala Cys Ile Ser Met Asp

E--> 362 arg tyr Ile ala Ile val gln ala thr Lys 130 135

W--> 363 140 tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag

W--> 364 gtc atc tgt 480Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile

E--> 365 cys 145 150 155 160

W--> 366 gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc 528Val Ala

W--> 367 Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile

W--> 368 165 170 175 ttc aac aag aaa tac gag

W--> 369 ctg cag gat cgt gat gtc tgt gag cca cgg 576Phe Asn Lys Lys Tyr Glu Leu Gln

E--> 370 asp arg asp val cys glu Pro arg 180 185

W--> 371 190 tac agg tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg

W--> 372 gga 624Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly

W--> 373 195 200 205 ctg gag ctg ttc

W--> 374 ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc 672Leu Glu Leu Phe Phe Gly

E--> 375 Phe Phe thr Pro Leu Leu Phe met val Phe 210 215

W--> 376 220 tgc tat ctg ttc att atc aag acc ttg gtg cag gcc cag

W--> 377 aac tcc aag 720Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser

E--> 378 Lys 225 230 235 240

W--> 379 agg cac aga gcc atc cga gtc gtg atc gct gtg gtt ctc gtg ttc ctg 768Arg His

W--> 380 Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

```

W--> 381 245                250                255                gct tgt cag atc cct cac
W--> 382 aac atg gtc ctc ctc gtg act gcg gtc aac                816Ala Cys Gln Ile Pro His Asn Met
E--> 383 val Leu Leu val thr ala val asn                260                265
W--> 384 270                acg ggc aaa gtg ggc cgg agc tgc acc gag aaa gtc ctc gcc
W--> 385 tac                864Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
W--> 386 275                280                285                acc agg aac gtg
W--> 387 gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac                912Thr Arg Asn Val Ala Glu
E--> 388 val Leu ala Phe Leu his cys cys Leu asn                290                295
W--> 389 300                ccc gtg ttg tat gcg ttt att gga cag aaa ttc aga aac
W--> 390 tac ttc atg                960Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe
E--> 391 met                305                310                315                320
W--> 392 aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct                1008Lys Ile
W--> 393 Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
W--> 394 325                330                335                ggc ttc ctc tgt gcc cgg
W--> 395 gtt tac tcg gaa agc tac atc tcc agg cag                1056Gly Phe Leu Cys Ala Arg Val Tyr
E--> 396 ser glu ser tyr Ile ser arg gln                340                345
W--> 397 350                acc agt gag acc gtc gaa aat gat aat gca tcg tcc ttt acc atg
W--> 398 1101Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
E--> 399 355                360                365
480 <210> SEQ ID NO: 13
481 <211> LENGTH: 1502
482 <212> TYPE: DNA
483 <213> ORGANISM: Rattus norvegicus (kidney)
485 <220> FEATURE:
486 <221> NAME/KEY: CDS
487 <222> LOCATION: (343)..(1443)
488 <223> OTHER INFORMATION:
W--> 490 <400> 13
E--> 491 tgtattgaag acagaacact tgttgtaaga caccacccc cgggagggcg aagaacaagc 60
W--> 492 60acacactgc tttgaagagt ccagcccca gcagaactgc aagggcagac actgttctgg
W--> 493 120acacctgcag tttgaagtca tcactttcaa tccccctgtg actagggcca gggctcttcac
W--> 494 180acctgcgaga ggaagcaaag atctaagcaa tctgaatttt aagagagaaa ctgcagctgt
W--> 495 240cggtttgtgg gccggaacat tattggactg gagcctggac aagcactaag gcgggggtac
E--> 496 300ctggccagcc cacttcggag ctacgcgttt ccttgggaaa cg atg aat ttc acc                354
E--> 497 met asn Phe thr                1
W--> 498 gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg                402Glu Ala
E--> 499 asn tyr gly met glu asp tyr thr gly ser asp tyr ser met                5
W--> 500 10                15                20                ttt cca gag acc gag cca tgc
W--> 501 tct ctg caa gag gtc aga gac ttc acc                450Phe Pro Glu Thr Glu Pro Cys Ser Leu
E--> 502 gln glu val arg asp Phe thr                25                30
W--> 503 35                aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc
W--> 504 498Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu
W--> 505 40                45                50                ctt ggc aat att atg
W--> 506 gtg gtg ata acc ttt gcc ttc tac aag aaa gcc                546Leu Gly Asn Ile Met Val Val
E--> 507 Ile thr Phe ala Phe tyr Lys Lys ala                55                60
W--> 508 65                agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca
W--> 509 gac ata                594Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile
W--> 510 70                75                80                ctc ttt gtc
W--> 511 ctc acc cta cca ttc tgg gca gtt act cat gcc act gac                642Leu Phe Val Leu Thr

```

*Cumulative base  
totals are at right  
margin of each line*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

*same*

```

E--> 512 Leu Pro Phe trp ala val thr his ala thr asp      85          90
W--> 513 95          100          act tgg atc ttt ggc aac acg atg tgt aaa ctg atg
W--> 514 aaa ggc acg tat      690Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly
E--> 515 thr tyr          105          110          115
W--> 516 gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg      738Ala Val
E--> 517 asn Phe asn cys gly met Leu Leu Leu ala cys Ile ser met          120
W--> 518 125          130          gac cgg tac att gcc atc gtc cag gcg acc
W--> 519 aaa tct ttc cgg gta cgc      786Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
E--> 520 Phe arg val arg          135          140          145
W--> 521 tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc      834Ser Arg
E--> 522 thr Leu thr his ser Lys val Ile cys Leu thr val trp Phe          150
W--> 523 155          160          gtt tcc atc atc atc tca agc ccc
W--> 524 aca ttc ttc ttc aac aag caa tac      882Val Ser Ile Ile Ile Ser Ser Pro Thr Phe
E--> 525 Phe Phe asn Lys gln tyr          165          170          175
W--> 526 180          aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg
W--> 527 930Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser
W--> 528 185          190          195          gag ccc atc acg tgg aaa
W--> 529 ctg ctg ggc atg gga ctc gag ctg ctc ttt      978Glu Pro Ile Thr Trp Lys Leu Leu
E--> 530 gly met gly Leu glu Leu Leu Phe          200          205
W--> 531 210          ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc
W--> 532 atc      1026Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile
W--> 533 215          220          225          atc aag acc ttg
W--> 534 gtg cag gcc cag aat tcc aag agg cac aga gcc atc      1074Ile Lys Thr Leu Val Gln
E--> 535 ala gln asn ser Lys arg his arg ala Ile          230          235
W--> 536 240          cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt
W--> 537 cag atc cct      1122Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile
E--> 538 Pro          245          250          255          260
W--> 539 cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc      1170His Asn
W--> 540 Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly
W--> 541 265          270          275          cgc agc tgc agc gcc gag
W--> 542 aaa gcc ctc gcc tac gcc agg aat gtg gct      1218Arg Ser Cys Ser Ala Glu Lys Ala
E--> 543 Leu ala tyr ala arg asn val ala          280          285
W--> 544 290          gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat
W--> 545 gcc      1266Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala
W--> 546 295          300          305          ttc att gga cag
W--> 547 aaa ttc aga agc tac ttc atg aag atc atg aag gat      1314Phe Ile Gly Gln Lys Phe
E--> 548 arg ser tyr Phe met Lys Ile met Lys asp          310          315
W--> 549 320          gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc
W--> 550 ttc tgt gcc      1362Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys
E--> 551 ala          325          330          335          340
W--> 552 cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta      1410Arg Val
W--> 553 Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val
W--> 554 345          350          355          gaa aat gac aac gca tcg
W--> 555 tcc ttt acc atg taa cagagagca caaagcagca      1463Glu Asn Asp Asn Ala Ser Ser Phe
E--> 556 thr met          360          365
E--> 557 tgccccgaaa gcctttgtga aacttgctat tacatgtga          1502
612 <210> SEQ ID NO: 15
613 <211> LENGTH: 1309
614 <212> TYPE: DNA

```



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

615 &lt;213&gt; ORGANISM: Rattus norvegicus (liver)

617 &lt;220&gt; FEATURE:

618 &lt;221&gt; NAME/KEY: CDS

619 &lt;222&gt; LOCATION: (150)..(1250)

620 &lt;223&gt; OTHER INFORMATION:

W--&gt; 622 &lt;400&gt; 15

E--&gt; 623 gcattctcact acccgctctct caatgagcac cgctgggtgt gcctgtcaac agaatagtcc

W--&gt; 624 60tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagccac

E--&gt; 625 120ttcggagctc agcgtttctt tgggaaacg atg aat ttc acc gag gcc aac tac 173

E--&gt; 626 met asn Phe thr glu ala asn tyr 1

W--&gt; 627 5 gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca

W--&gt; 628 gag acc 221Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr

W--&gt; 629 10 15 20 gag cca tgc

W--&gt; 630 tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg 269Glu Pro Cys Ser Leu

E--&gt; 631 gln glu val arg asp Phe thr Lys val Phe val 25 30

W--&gt; 632 35 40 cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc

W--&gt; 633 ctt ggc aat att 317Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly

E--&gt; 634 asn Ile 45 50 55

W--&gt; 635 atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act 365Met Val

E--&gt; 636 val Ile thr Phe ala Phe tyr Lys Lys ala arg ser met thr 60

W--&gt; 637 65 70 gac gtc tac cta ttg aac atg gcc atc aca

W--&gt; 638 gac ata ctc ttt gtc ctc 413Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile

E--&gt; 639 Leu Phe val Leu 75 80 85

W--&gt; 640 acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt 461Thr Leu

E--&gt; 641 Pro Phe trp ala val thr his ala thr asp thr trp Ile Phe 90

W--&gt; 642 95 100 ggc aac acg atg tgt aaa ctg atg

W--&gt; 643 aaa ggc acg tat gcg gtc aac ttt 509Gly Asn Thr Met Cys Lys Leu Met Lys Gly

E--&gt; 644 thr tyr ala val asn Phe 105 110 115

W--&gt; 645 120 aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att

W--&gt; 646 557Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile

W--&gt; 647 125 130 135 gcc atc gtc cag gcg acc

W--&gt; 648 aaa tct ttc cgg gta cgc tcc aga aca ctg 605Ala Ile Val Gln Ala Thr Lys Ser

E--&gt; 649 Phe arg val arg ser arg thr Leu 140 145

W--&gt; 650 150 acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc

W--&gt; 651 atc 653Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile

W--&gt; 652 155 160 165 atc tca agc ccc

W--&gt; 653 aca ttc ttc ttc aac aag caa tac aag ctg cag ggc 701Ile Ser Ser Pro Thr Phe

E--&gt; 654 Phe Phe asn Lys gln tyr Lys Leu gln gly 170 175

W--&gt; 655 180 cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg gag

W--&gt; 656 ccc atc acg 749Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile

E--&gt; 657 thr 185 190 195 200

W--&gt; 658 tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc 797Trp Lys

W--&gt; 659 Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile

W--&gt; 660 205 210 215 cct ttg ctg ttt atg gtg

W--&gt; 661 ttc tgt tac ctg ttc atc atc aag acc ttg 845Pro Leu Leu Phe Met Val Phe Cys

E--&gt; 662 tyr Leu Phe Ile Ile Lys thr Leu 220 225

W--&gt; 663 230 gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg

W--&gt; 664 att 893Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile

W--&gt; 665 235 240 245 gct gtg gtt ctc

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,532

TIME: 13:24:41

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

*some*

```

W--> 666 gtg ttc ctg gct tgt cag atc cct cac aac atg gtc      941Ala Val Val Leu Val Phe
E--> 667 Leu ala cys gln Ile Pro his asn met val      250      255
W--> 668 260      ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc
W--> 669 agc tgc agc      989Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys
E--> 670 ser      265      270      275      280
W--> 671 gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct      1037Ala Glu
W--> 672 Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala
W--> 673 285      290      295      ttc ctg cac tgc tgt ctc
W--> 674 aac ccc gtg ttg tat gcc ttc att gga cag      1085Phe Leu His Cys Cys Leu Asn Pro
E--> 675 val Leu tyr ala Phe Ile gly gln      300      305
W--> 676 310      aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt
W--> 677 atg      1133Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met
W--> 678 315      320      325      agg agg aag agc
W--> 679 aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca      1181Arg Arg Lys Ser Lys Val
E--> 680 Pro thr Phe Phe cys ala arg val tyr ser      330      335
W--> 681 340      gaa agc tac atc tcc agg cag acc agt gag act gta gaa
W--> 682 aat gac aac      1229Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp
E--> 683 asn      345      350      355      360
W--> 684 gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa      1280Ala Ser
W--> 685 Ser Phe Thr Met
W--> 686 365
E--> 687 tacatgtga      1309      gcctttgtga aacttgctat

```

10/547,532 10

<210> 11  
<211> 20  
<212> DNA  
<213> Artificial

<220>

<221> misc\_feature

<223> Oligonucleotide designed to act as primer for amplifying fragment  
of rat MIP-3*fi* gene transcript.

do NOT use scientific symbols or foreign accent  
marks

↓ global  
error

(They cannot be  
processed by CLF  
software.)

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005  
TIME: 13:24:42

Input Set : A:\PTO.AMC.txt  
Output Set : N:\CRF4\09132005\J547532.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 47,48,49,50,51,52,53,54,55,56,57,59,60,61  
Seq#:3; Line(s) 104,105,107,108,109,110,111,112,113,114,115,116,117,118,119  
Seq#:5; Line(s) 161,162,163,164,165,166,167,168,169,170,171,172,173,174,175  
Seq#:5; Line(s) 176,177  
Seq#:7; Line(s) 211,212,213,214,215,216,217,218,219,220,221,222,223,224,225  
Seq#:7; Line(s) 226,227,228,229,230,231,232,233,234,235,236,237,238,239,240  
Seq#:7; Line(s) 241,242,243,244,245,246,247,248,249,250,251,252,253,254,255  
Seq#:7; Line(s) 256,257,258,259,260,261,262,263,264,265,266,267,268,269,270  
Seq#:7; Line(s) 271  
Seq#:9; Line(s) 340,341,342,343,344,345,346,347,348,349,350,351,352,353,354  
Seq#:9; Line(s) 355,356,357,358,359,360,361,362,363,364,365,366,367,368,369  
Seq#:9; Line(s) 370,371,372,373,374,375,376,377,378,379,380,381,382,383,384  
Seq#:9; Line(s) 385,386,387,388,389,390,391,392,393,394,395,396,397,398  
Seq#:13; Line(s) 496,497,498,499,500,501,502,503,504,505,506,507,508,509  
Seq#:13; Line(s) 510,511,512,513,514,515,516,517,518,519,520,521,522,523  
Seq#:13; Line(s) 524,525,526,527,528,529,530,531,532,533,534,535,536,537  
Seq#:13; Line(s) 538,539,540,541,542,543,544,545,546,547,548,549,550,551  
Seq#:13; Line(s) 552,553,554,555,556  
Seq#:15; Line(s) 625,626,627,628,629,630,631,632,633,634,635,636,637,638  
Seq#:15; Line(s) 639,640,641,642,643,644,645,646,647,648,649,650,651,652  
Seq#:15; Line(s) 653,654,655,656,657,658,659,660,661,662,663,664,665,666  
Seq#:15; Line(s) 667,668,669,670,671,672,673,674,675,676,677,678,679,680  
Seq#:15; Line(s) 681,682,683,684,685

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,16,17,18,19,20,21

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:34  
 L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:39  
 L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:44  
 L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:48 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:1  
 L:48 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:48 M:112 C: (48) String data converted to lower case,  
 L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:50 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:25  
 L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 M:254 Repeated in SeqNo=1  
 L:51 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5  
 M:112 Repeated in SeqNo=1  
 L:52 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:53 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
 L:54 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:54 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:55 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12  
 M:341 Repeated in SeqNo=1  
 L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:56 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13  
 L:57 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15  
 L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:58 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:59 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
 L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15  
 L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
 L:61 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14  
 L:62 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:127 SEQ:1  
 L:98 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:91  
 L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:96  
 L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:101  
 L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:105 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:3  
 L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:20  
 L:105 M:112 C: (48) String data converted to lower case,  
 M:254 Repeated in SeqNo=3  
 L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10  
 L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:22  
 L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
 M:112 Repeated in SeqNo=3  
 L:112 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15  
 L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6  
 L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14  
 M:341 Repeated in SeqNo=3  
 L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:116 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
 L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14  
 L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:118 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
 L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
 L:119 M:252 E: No. of Seq. differs, <211> LENGTH:Input:288 Found:106 SEQ:3  
 L:155 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:148  
 L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:153  
 L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:158  
 L:161 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:162 M:254 E: No. of Bases conflict, LENGTH:Input:-25 Counted:43 SEQ:5  
 L:162 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:162 M:112 C: (48) String data converted to lower case,  
 L:163 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:164 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:25  
 L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 M:254 Repeated in SeqNo=5  
 L:165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
 M:112 Repeated in SeqNo=5  
 L:166 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:167 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
 L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:168 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 M:341 Repeated in SeqNo=5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:170 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
 L:171 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
 L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:172 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
 L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13  
 L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:175 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:176 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4  
 L:177 M:252 E: No. of Seq. differs, <211> LENGTH:Input:291 Found:118 SEQ:5  
 L:210 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:208  
 L:211 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
 L:212 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:7  
 L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15  
 L:212 M:112 C: (48) String data converted to lower case,  
 L:213 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:214 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 M:254 Repeated in SeqNo=7  
 L:215 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
 M:112 Repeated in SeqNo=7  
 L:216 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
 L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:217 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
 L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:219 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13  
 M:341 Repeated in SeqNo=7  
 L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:220 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14  
 L:221 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14  
 L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:222 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:223 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:224 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:17  
 L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:226 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9  
 L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

L:227 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:228 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
 L:229 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
 L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:230 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2  
 L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:231 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
 L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
 L:232 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13  
 L:233 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
 L:234 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14  
 L:241 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5  
 L:246 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:254 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 L:259 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
 L:262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:267 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
 L:272 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1122 Found:294 SEQ:7  
 L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:337  
 L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
 L:341 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:42 SEQ:9  
 L:341 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 L:341 M:112 C: (48) String data converted to lower case,  
 M:254 Repeated in SeqNo=9  
 L:344 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 M:112 Repeated in SeqNo=9  
 M:341 Repeated in SeqNo=9  
 L:349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:352 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:357 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:10  
 L:362 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
 L:375 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16  
 L:378 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:383 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
 L:388 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:391 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
 L:396 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
 L:399 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1101 Found:294 SEQ:9  
 L:490 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:488  
 L:491 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13  
 M:254 Repeated in SeqNo=13  
 L:496 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
 M:341 Repeated in SeqNo=13  
 L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
 M:112 Repeated in SeqNo=13  
 L:499 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
 L:502 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/547,532

DATE: 09/13/2005

TIME: 13:24:42

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\09132005\J547532.raw

L:507 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
L:512 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:517 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:16  
L:520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:522 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15  
L:525 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
L:530 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:535 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9  
L:557 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1502 Found:528 SEQ:13  
L:622 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:620  
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15  
M:254 Repeated in SeqNo=15  
M:341 Repeated in SeqNo=15  
M:112 Repeated in SeqNo=15  
L:687 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1309 Found:470 SEQ:15